

WO 2005/037989

PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 ggctcgggcg gtggtgggtc ggggtggcggc ggatcggtcac aggtgcagct gaagcagtc 480
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 tcattaacta cctatgctgt acactgggtt cgccagcttc caggaaagg tctggagtgg 600
 ctgggagtga tatggagtgg tggaaacaca gactataatg cagctttcat atccagactg 660
 agcatcacca aggacgattc caagagccaa gttttcttta aaatgaacag tctgcaacct 720
 aatgacacag ccatttatta ctgtgccaga aatgggggtg ataactaccc ttattactat 780
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<210> 357
 <211> 1536
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

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 acatcagctt ccattctctg cagggtctagt aagagtctcc tacatagtaa tggcatcact 180
 tatattgtatt ggtatctgca gaagccaggc cagtctcctc agctcctgat ttatcagatg 240
 tccaaccttg cctcaggagt ccagacagg ttcagtagca gtgggtcagg aactgatttc 300
 acactgagaa tcagcagagt ggaggctgag gatgtgggtg ttattactg tgctcaaaat 360
 ctagaacttc cgctcacgtt cgggtgctggg accaagctgg agctgaaacg ggggtggcgg 420
 ggctcgggcg gtggtgggtc ggggtggcggc ggatcggtcac aggtgcagct gaagcagtc 480
 ggacctggcc tagtgcagtc ctacagagc ctgtccatca cctgcacagt ctctggtttc 540
 tcattaacta cctatgctgt acactgggtt cgccagcttc caggaaagg tctggagtgg 600
 ctgggagtga tatggagtgg tggaaacaca gactataatg cagctttcat atccagactg 660
 agcatcacca aggacgattc caagagccaa gttttcttta aaatgaacag tctgcaacct 720
 aatgacacag ccatttatta ctgtgccaga aatgggggtg ataactaccc ttattactat 780
 gctatggact actgggggtca aggaacctca gtcaccgtct cctctgatca ggagccaaa 840
 tcttctgaca aaactcacac atccccaccg tccccagcac ctgaactcct ggggggaccg 900
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 accaagaacc aggtcagcct gacctgctg gtcaaaggct tctatcccag cgacatcgcc 1320
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 gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440
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 aagagcctct ccctgtctcc gggtaaatga tctaga 1536

<210> 358
 <211> 1696
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 358
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 acatcagctt ccattctctg cagggtctagt aagagtctcc tacatagtaa tggcatcact 180
 tatattgtatt ggtatctgca gaagccaggc cagtctcctc agctcctgat ttatcagatg 240
 tccaaccttg cctcaggagt ccagacagg ttcagtagca gtgggtcagg aactgatttc 300
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 ctagaacttc cgctcacgtt cgggtgctggg accaagctgg agctgaaacg ggggtggcgg 420
 ggctcgggcg gtggtgggtc ggggtggcggc ggatcggtcac aggtgcagct gaagcagtc 480
 ggacctggcc tagtgcagtc ctacagagc ctgtccatca cctgcacagt ctctggtttc 540
 tcattaacta cctatgctgt acactgggtt cgccagcttc caggaaagg tctggagtgg 600
 ctgggagtga tatggagtgg tggaaacaca gactataatg cagctttcat atccagactg 660
 agcatcacca aggacgattc caagagccaa gttttcttta aaatgaacag tctgcaacct 720
 aatgacacag ccatttatta ctgtgccaga aatgggggtg ataactaccc ttattactat 780
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 tcttctgaca aaactcacac aagccccaccg agcccagcac ctgaactcct ggggggacg 900
 tcagtcttcc tcttcccccc aaaacccaag gacacctca tgatctccc gaccttgag 960

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
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 tacaagtgca aggtctccaa caaagccctc ccagcccca tcgagaaaac catctccaaa 1200
 gccaaaggcg agcccgaga accacaggtg tacaccctgc ccccatcccg ggatgagctg 1260
 accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctatcccag cgacatcgcc 1320
 gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg 1380
 gactccgacg gctccttctt cctctacagc aagctcaccg tggacaagag caggtggcag 1440
 caggggaacg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacgcag 1500
 aagagcctct ccctgtctcc gggtaaagcg gatccttcga acctgctccc atcctgggcc 1560
 attaccttaa tctcagtaaa tggaattttt gtgatatgct gcctgaccta ctgctttgcc 1620
 ccaagatgca gagagagaag gaggaatgag agattgagaa gggaaagtgt acgcctctga 1680
 taaatcgata ctcgag 1696

<210> 359
 <211> 141
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 359
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 1 5 10 15
 Val Leu Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln
 20 25 30
 Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
 35 40 45
 Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala
 65 70 75 80
 Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys Ser Gln
 85 90 95
 Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr
 100 105 110
 Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr Ala Met
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 130 135 140

<210> 360
 <211> 122
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 360
 Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu Val Gln Ser Ser Gln
 1 5 10 15
 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr
 20 25 30
 Ala Val His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Leu
 35 40 45
 Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr Asn Ala Ala Phe Ile
 50 55 60
 Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys Ser Gln Val Phe Phe
 65 70 75 80
 Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala Ile Tyr Tyr Cys Ala
 85 90 95
 Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr Ala Met Asp Tyr Trp
 100 105 110
 Gly Gln Gly Thr Ser Val Thr Val Ser Ser

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
115 120

<210> 361
<211> 133
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 361
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg
130

<210> 362
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 362
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
20 25 30
Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Lys Ser
35 40 45
Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
50 55 60
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
65 70 75 80
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
85 90 95
Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110
Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
115 120 125
Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly
130 135 140
Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
145 150 155 160
Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
165 170 175
Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
180 185 190
Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
195 200 205

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
 210 215 220
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
 225 230 235 240
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
 245 250 255
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser
 260 265 270

<210> 363
 <211> 505
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 363
 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
 1 5 10 15
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
 20 25 30
 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
 35 40 45
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 50 55 60
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 85 90 95
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 105 110
 Cys Ala Gln Asn Leu Glu Leu Pro Thr Phe Gly Ala Gly Thr Lys
 115 120 125
 Leu Glu Leu Lys Arg Gly Gly Gly Ser Gly Gly Gly Ser Gly
 130 135 140
 Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
 145 150 155 160
 Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
 165 170 175
 Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
 180 185 190
 Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
 195 200 205
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
 210 215 220
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
 225 230 235 240
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
 245 250 255
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 265 270
 Gln Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Ser Pro
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 330 335
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 340 345 350
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 355 360 365
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 370 375 380
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 385 390 395 400
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 405 410 415
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 420 425 430
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 435 440 445
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 450 455 460
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 465 470 475 480
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 485 490 495
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 500 505

<210> 364
 <211> 556
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 364
 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
 1 5 10 15
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ala Ala Phe Ser Asn Pro
 20 25 30
 Val Thr Leu Gly Thr Ser Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
 35 40 45
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 50 55 60
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
 65 70 75 80
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 85 90 95
 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 100 105 110
 Cys Ala Gln Asn Leu Glu Leu Pro Leu Thr Phe Gly Ala Gly Thr Lys
 115 120 125
 Leu Glu Leu Lys Arg Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly
 130 135 140
 Gly Gly Gly Ser Ser Gln Val Gln Leu Lys Gln Ser Gly Pro Gly Leu
 145 150 155 160
 Val Gln Ser Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe
 165 170 175
 Ser Leu Thr Thr Tyr Ala Val His Trp Val Arg Gln Ser Pro Gly Lys
 180 185 190
 Gly Leu Glu Trp Leu Gly Val Ile Trp Ser Gly Gly Ile Thr Asp Tyr
 195 200 205
 Asn Ala Ala Phe Ile Ser Arg Leu Ser Ile Thr Lys Asp Asp Ser Lys
 210 215 220
 Ser Gln Val Phe Phe Lys Met Asn Ser Leu Gln Pro Asn Asp Thr Ala
 225 230 235 240
 Ile Tyr Tyr Cys Ala Arg Asn Gly Gly Asp Asn Tyr Pro Tyr Tyr Tyr
 245 250 255
 Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Asp
 260 265 270
 Leu Glu Pro Lys Ser Ser Asp Lys Thr His Thr Ser Pro Ser Pro
 275 280 285
 Ala Pro Glu Leu Leu Gly Gly Ser Ser Val Phe Leu Phe Pro Pro Lys
 290 295 300
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 305 310 315 320
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 325 330 335

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
340 345 350
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
355 360 365
Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
370 375 380
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
385 390 395 400
Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
405 410 415
Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
420 425 430
Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
435 440 445
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
450 455 460
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
465 470 475 480
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
485 490 495
Lys Ser Leu Ser Leu Ser Pro Gly Lys Ala Asp Pro Ser Asn Leu Leu
500 505 510
Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly Ile Phe Val Ile
515 520 525
Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg
530 535 540
Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
545 550 555

<210> 365
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
405 XX to Y

<400> 365
gttggtgaag acgttcccct gctgccacct gctcttgtcc acggtgagct tgctgtagag 60
gtagaaggag cc 72

<210> 366
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
405 XX to A

<400> 366
gttggtgaag acgttcccct gctgccacct gctcttgtcc acggtgagct tgctgtagag 60
ggcgaaggag cc 72

<210> 367
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
407 XX to A

<400> 367

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
gttggtgaag acgttcccct gctgccacct gctcttgcc acggtgagct tgctggcgag 60
gaagaaggag cc 72

<210> 368
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
405 XX to Y and 407 to A

<400> 368
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gtagaaggag cc 72

<210> 369
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligo to introduce mutation in CH3 at position
405 XX to A and 407 to Y

<400> 369
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ggcgaaggag cc 72

<210> 370
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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aaccaggtca gcctgacctg cctggtcaaa ggcttctatc ccagcgacat cgccgtggag 120
tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 180
gacggctcct tctacctcta tagcaagctc accgtggaca agagcagggtg gcagcagggg 240
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300
ctctccctgt ccccggttaa atga 324

<210> 371
<211> 324
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 371
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tgggagagca atgggcagcc ggagaacaac tacaagacca cgctcccgt gctggactcc 180
gacggctcct tcgacctcta tagcaagctc accgtggaca agagcagggtg gcagcagggg 240
aacgtcttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300
ctctccctgt ccccggttaa atga 324

<210> 372
<211> 324
<212> DNA
<213> Artificial Sequence

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<220>

<223> fusion polynucleotide

<400> 372

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tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgctccccgt	gctggactcc	180
gacggctcct	tcttcctcgc	cagcaagctc	accgtggaca	agagcagggtg	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
ctctccctgt	ccccgggtaa	atga				324

<210> 373

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 373

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tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgctccccgt	gctggactcc	180
gacggctcct	tcttcctcgc	cagcaagctc	accgtggaca	agagcagggtg	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
ctctccctgt	ccccgggtaa	atga				324

<210> 374

<211> 324

<212> DNA

<213> Artificial Sequence

<220>

<223> fusion polynucleotide

<400> 374

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tgggagagca	atgggcagcc	ggagaacaac	tacaagacca	cgctccccgt	gctggactcc	180
gacggctcct	tcgccctcgc	cagcaagctc	accgtggaca	agagcagggtg	gcagcagggg	240
aacgtcttct	catgctccgt	gatgcatgag	gctctgcaca	accactacac	gcagaagagc	300
ctctccctgt	ccccgggtaa	atga				324

<210> 375

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 375

Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu
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Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
			20					25					30		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
			35				40					45			
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	50					55				60					
Tyr	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
65					70					75				80	
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
				85					90				95		

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 376
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 376
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Ala Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 377
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 377
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
20 25 30
Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
35 40 45
Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
50 55 60
Phe Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
65 70 75 80
Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
85 90 95
Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
100 105

<210> 378
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 378
Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
1 5 10 15
Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe

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 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 20 25 30
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 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
 40 45
 50
 Tyr Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 55 60
 65
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 70 75 80
 85
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 90 95
 100 105

<210> 379
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 379
 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 1 5 10 15
 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 20 25 30
 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 35 40 45
 Asn Asn Tyr Lys Thr Thr Pro Val Leu Asp Ser Asp Gly Ser Phe
 50 55 60
 Ala Leu Ala Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
 65 70 75 80
 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
 85 90 95
 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 100 105

<210> 380
 <211> 1515
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 380
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 gtcataattg ccagaggaca aattgtttct tcccagttct cagcaatcct gtctgcatct 120
 ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcaactg 180
 taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctgggt 240
 tctggagtcc ctgctcgctt cagtggcagt gggctctgga cctcttactc tctcacaatc 300
 agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
 cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
 aggcctgggg cctcagtga gattgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgct 720
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgt 780
 ggcacagggg ccacggtcac cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840
 cacacatccc caccgtcccc agcacctgaa ctctctgggg gaccgtcagt ctctctcttc 900
 ccccctgagc ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgcgtgggt 960
 gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
 gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggt 1080
 agcgtctcca ccgtctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140

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 agcctgacct gcctgggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1320
 aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
 ttctgacctt atagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
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 tccccgggta aatga 1515

<210> 381
 <211> 1521
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

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 ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcaactg 180
 taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
 tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
 agcagagtgg aggttgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
 cccacgttcg gtgctgggac caagctggag ctctcaggct tatctacagc agtctggggc tgagctgggt 420
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
 aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgcg 720
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg 780
 ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaactctc tgacaaaact 840
 cacacatccc caccgtcccc agcacctgaa ctccctggggg gaccgtcagt cttcctcttc 900
 cccccaaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgctgtggg 960
 gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
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 agcgtcctca cgtctctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140
 tccaacaaag ccctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
 cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggctc 1260
 agcctgacct gcctgggtcaa aggcttctat cccagcgaca tcgccgtgga gtgggagagc 1320
 aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
 ttctacctct atagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
 tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
 tccccgggta aatgatctag a 1521

<210> 382
 <211> 1515
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> fusion polynucleotide

<400> 382
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 ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcaactg 180
 taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
 tctggagtcc ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
 agcagagtgg aggttgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
 cccacgttcg gtgctgggac caagctggag ctctcaggct tatctacagc agtctggggc tgagctgggt 420
 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggt 480
 aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctacagcagc tgacatctga agactctgcg 720

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ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaactctt tgacaaaact 840
cacacatccc caccgtcccc agcacctgaa ctccctgggg gaccgtcagt ctccctcttc 900
ccccaaaaac ccaaggacac cctcatgac tcccggaccc ctgaggtcac atgctgtggtg 960
gtggacgtga gccacgaaga cctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
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ttcttctctg ccagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgtcccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
tccccgggta aatga 1515
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<210> 383
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgactgtg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggctctgga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaacca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcgtgggt 420
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aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatactc ctacaatcag aagtcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaactctt tgacaaaact 840
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gtggacgtga gccacgaaga cctgaggtc aagttcaact ggtacgtgga cggcgtggag 1020
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agcctgacct gcctggtcaa aggtcttat cccagcgaca tcgccgtgga gtgggagagc 1320
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ttctacctcg ccagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
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tccccgggta aatga 1515
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<210> 384
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

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ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgactgtg 180
taccagcaga agccaggatc ctccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggctctgga cctcttactc tctcacaatc 300
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 ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
 aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
 aatattgact gggtaaaagca gacacctaga cagggccttg aatggattgg agctatttat 600
 ccaggaaatg gtgatacttc ctacaatcag aagtccaagg gcaaggccac actgactgta 660
 gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgctg 720
 gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
 ggcacagggg ccaagggtcac cgtctcttct gatcaggagc ccaaactctt tgacaaaact 840
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 agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140
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 cgagaaccac aggtgtacac cctgccccca tcccgggagg agatgaccaa gaaccaggtc 1260
 agcctgacct gcctgggtcaa aggccttctat cccagcgaca tcgccgtgga gtgggagagc 1320
 aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacggctcc 1380
 ttcgccctcg ccagcaagct caccgtggac aagagcaggt ggacgaggg gaacgtcttc 1440
 tcatgtctcg tgatgcatga ggctctgcac aaccactaca cgagaagag cctctccctg 1500
 tccccgggta aatga 1515

<210> 385
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 385
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285

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 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 386
 <211> 500
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion polypeptide

<400> 386
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220

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 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 387
 <211> 500
 <212> PRT
 <213> Artificial sequence

<220>
 <223> fusion polypeptide

<400> 387
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 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160

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 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 388
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 388
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Tyr Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 389
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 389
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30

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49076.000004pct2.10.207.655 Seq List Text 07.24.03.txt
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Ser Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Ala Leu Ala Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 390
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 5' oligo to mutat IgG1

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<400> 390
gttggtgac aggagcccaa atcttctgac aaaactcaca catg 44

<210> 391
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to mutate IgG1

<400> 391
gttggtgac aggagcccaa atcttctgac aaaactcaca catctccacc gtgc 54

<210> 392
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligo to mutate IgG1

<400> 392
gttggtgac aggagcccaa atcttctgac aaaactcaca catgtccacc gtccccagca 60
cct 63

<210> 393
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 393
aagcttgccg ccatggattt tcaagtgcag attttcagct tcctgctaata cagtgccttca 60
gtcataattg ccagaggaca aattgttctc tcccagctctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa ccttggattt atgccccatc caacctggct 240
tctggagtcg ctgctcgctt cagtggcagt gggctctggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tttactgccc agcagtgagg ttttaaccca 360
cccacgttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaagca gacacctaga cagggccttg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgag 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actggtactt cgatgtctgg 780
ggcacaggga ccacggtcac cgtctcttct gatcaggagc ccaaatcttc tgacaaaact 840
cacacatgcc caccgtgccc agcacctgaa ctcttggggg gaccgtcagt cttcctcttc 900
ccccaaaac ccaaggacac cctcatgac tcccggacc ctgaggtcac atgctgggtg 960
gtggacgtga gccacgaaga ccctgaggtc aagttcaact ggtacgtgga cggcggtggag 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080
agcgtcctca ccgtcctgca ccagactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
tccaacaaag ccctcccagc ccccatcgag aaaacaatct tcccgggatg agctgaccaa gaaccaggtc 1260
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260
agcctgacct gcctgggtcaa aggtcttctat cccagcgaca tcgcccgtga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgctctccg tgctggactc cgacggcttc 1380
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500

WO 2005/037989

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
tctccgggta aatgatctag a

1521

<210> 394
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 394
aagcttgccg ccattggattt tcaagtgcag attttcagct tcctgctaatt cagtgccttca 60
gtcataaattg ccagaggaca aattgttctc tcccagtcctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggctcggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
ccacggttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg 780
ggcacagggg ccccggtcac cgtctcttct gatcaggagc ccaaactctg tgacaaaact 840
cacacatctc caccgtgccc agcacctgaa ctctggggg gaccgtcagt cttcctcttc 900
cccccaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgctgtggg 960
gtggacgtga gccacgaaga ccctgagggtc aagttcaact ggtacgtgga cggcggtggg 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080
agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaagggtc 1140
tccaacaaag cctcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccagggtc 1260
agcctgacct gcctgggtcaa aggttcttat cccagcagca tcgcccgtgga gtgggagagc 1320
aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacgggtcc 1380
ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
tcattgctcc tgatgcata ggtctgcac aaccactaca cgcagaagag cctctccctg 1500
tctccgggta aatgatctag a

<210> 395
<211> 1521
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 395
aagcttgccg ccattggattt tcaagtgcag attttcagct tcctgctaatt cagtgccttca 60
gtcataaattg ccagaggaca aattgttctc tcccagtcctc cagcaatcct gtctgcatct 120
ccaggggaga aggtcacaat gacttgcagg gccagctcaa gtgtaagtta catgcactgg 180
taccagcaga agccaggatc ctcccccaaa ccctggattt atgccccatc caacctggct 240
tctggagtcc ctgctcgctt cagtggcagt gggctcggga cctcttactc tctcacaatc 300
agcagagtgg aggtgaaga tgctgccact tattactgcc agcagtggag ttttaaccca 360
ccacggttcg gtgctgggac caagctggag ctgaaagatg gcggtggctc gggcggtggg 420
ggatctggag gaggtgggag ctctcaggct tatctacagc agtctggggc tgagctgggtg 480
aggcctgggg cctcagtga gatgtcctgc aaggcttctg gctacacatt taccagttac 540
aatatgcact gggtaaaagca gacacctaga cagggcctgg aatggattgg agctatttat 600
ccaggaaatg gtgatacttc ctacaatcag aagttcaagg gcaaggccac actgactgta 660
gacaaatcct ccagcacagc ctacatgcag ctacagagcc tgacatctga agactctgcg 720
gtctatttct gtgcaagagt ggtgtactat agtaactctt actgggtactt cgatgtctgg 780
ggcacagggg ccccggtcac cgtctcttct gatcaggagc ccaaactctg tgacaaaact 840
cacacatgct caccgtcccc agcacctgaa ctctggggg gaccgtcagt cttcctcttc 900
cccccaaac ccaaggacac cctcatgatc tcccggaccc ctgaggtcac atgctgtggg 960
gtggacgtga gccacgaaga ccctgagggtc aagttcaact ggtacgtgga cggcggtggg 1020
gtgcataatg ccaagacaaa gccgcgggag gagcagtaca acagcacgta ccgtgtgggtc 1080

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 agcgtcctca ccgtcctgca ccaggactgg ctgaatggca aggagtacaa gtgcaaggtc 1140
 tccaacaaag ccttcccagc ccccatcgag aaaacaatct ccaaagccaa agggcagccc 1200
 cgagaaccac aggtgtacac cctgccccca tcccgggatg agctgaccaa gaaccaggtc 1260
 agcctgacct gcctgggtcaa aggtcttctat cccagcgaca tcgccgtgga gtgggagagc 1320
 aatgggcagc cggagaacaa ctacaagacc acgcctcccg tgctggactc cgacgggtcc 1380
 ttcttctctt acagcaagct caccgtggac aagagcaggt ggcagcaggg gaacgtcttc 1440
 tcatgctccg tgatgcatga ggctctgcac aaccactaca cgcagaagag cctctccctg 1500
 tctccgggta aatgatctag a 1521

<210> 396
 <211> 500
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> fusion polypeptide

<400> 396
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
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 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Ser Asp Lys Thr His Thr Cys Pro Cys Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 385 390 395 400
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 397
 <211> 500
 <212> PRT
 <213> Artificial sequence

<220>
 <223> fusion polypeptide

<400> 397
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 1 5 10 15
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 20 25 30
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 35 40 45
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 50 55 60
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 65 70 75 80
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 85 90 95
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 100 105 110
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 115 120 125
 Asp Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 130 135 140
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 145 150 155 160
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 165 170 175
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 180 185 190
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 195 200 205
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 210 215 220
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 225 230 235 240
 Ala Arg Val Val Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 245 250 255
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 260 265 270
 Cys Asp Lys Thr His Thr Ser Pro Cys Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 Ser Pro Gly Lys
 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500

<210> 398
 <211> 500
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion polypeptide

<400> 398
 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
 Val Ile Ile Ala Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
 Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Ser Ser
 Pro Lys Pro Trp Ile Tyr Ala Pro Ser Asn Leu Ala Ser Gly Val Pro
 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
 Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
 Ser Phe Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
 Asp Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ser
 Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg Pro Gly Ala
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu Glu Trp Ile
 Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Ala Tyr
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys
 Ala Arg Val Val Tyr Tyr Ser Asn Ser Tyr Trp Tyr Phe Asp Val Trp
 Gly Thr Gly Thr Thr Val Thr Val Ser Ser Asp Gln Glu Pro Lys Ser
 1 5 10 15 20 25 30 35 40 45 50 55 60 65 70 75 80 85 90 95 100 105 110 115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255

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PCT/US2003/024918

49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt
 260 265 270
 Cys Asp Lys Thr His Thr Cys Pro Ser Pro Ala Pro Glu Leu Leu
 275 280 285
 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 290 295 300
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Asp Val Ser
 305 310 315 320
 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
 325 330 335
 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
 340 345 350
 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
 355 360 365
 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
 370 375 380
 Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
 385 390 395 400
 Val Tyr Thr Leu Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
 405 410 415
 Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 420 425 430
 Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 435 440 445
 Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 450 455 460
 Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 465 470 475 480
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 485 490 495
 Ser Pro Gly Lys
 500

<210> 399
 <211> 793
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> fusion polynucleotide

<400> 399
 atgttgata catctcagct ccttgggctt ttactcttct ggatttcagc ctccagaagt 60
 gacatagtgc tgactcagac tccagccact ctgtctctaa ttcctggaga aagagtcaca 120
 atgacctgta agaccagtca gaatatgggc acaatcttac actggtatca ccaaaaacca 180
 aaggaggctc caagggtctc catcaagtat gcttcgcagt ccattcctgg gatcccctcc 240
 agattcagtg gcagtggttc ggaaacagat ttcactctca gcatcaataa cctggagcct 300
 gatgatatcg gaatttatta ctgtcaacaa agtagaagct ggcctgtcac gttcggctct 360
 ggcaccaagc tggagataaa acgggggtggc ggtggctcgg gcggaggtgg gtcgggtggc 420
 ggcggatctc aggtcaagct gcagcagctc ggttctgaac tagggaaacc tggggcctca 480
 gtgaaactgt cctgcaagac ttcaggctac atattcacag atcactatat ttcttgggtg 540
 aaacagaagc ctggagaaag cctgcagtgg ataggaaatg tttatgggtg aaatggtgg 600
 acaagctaca atcaaaaatt ccagggcaag gccacactga ctgtagataa aatctctagc 660
 acagcctaca tggaaactcag cagcctgaca tctgaggatt ctgccatcta ttactgtgca 720
 agaaggccgg tagcgacggg ccatgctatg gactactggg gtcaggggat ccaagttacc 780
 gtctcctctg atc
 793

<210> 400
 <211> 264
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> fusion polypeptide

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<400> 400
Met Leu Tyr Thr Ser Gln Leu Leu Gly Leu Leu Phe Trp Ile Ser
1 5 10 15
Ala Ser Arg Ser Asp Ile Val Leu Thr Gln Thr Pro Ala Thr Leu Ser
20 25 30
Leu Ile Pro Gly Glu Arg Val Thr Met Thr Cys Lys Thr Ser Gln Asn
35 40 45
Ile Gly Thr Ile Leu His Trp Tyr His Gln Lys Pro Lys Glu Ala Pro
50 55 60
Arg Ala Leu Ile Lys Tyr Ala Ser Gln Ser Ile Pro Gly Ile Pro Ser
65 70 75 80
Arg Phe Ser Gly Ser Gly Ser Glu Thr Asp Phe Thr Leu Ser Ile Asn
85 90 95
Asn Leu Glu Pro Asp Asp Ile Gly Ile Tyr Tyr Cys Gln Gln Ser Arg
100 105 110
Ser Trp Pro Val Thr Phe Gly Pro Gly Thr Lys Leu Glu Ile Lys Arg
115 120 125
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gln
130 135 140
Val Lys Leu Gln Gln Ser Gly Ser Glu Leu Gly Lys Pro Gly Ala Ser
145 150 155 160
Val Lys Leu Ser Cys Lys Thr Ser Gly Tyr Ile Phe Thr Asp His Tyr
165 170 175
Ile Ser Trp Val Lys Gln Lys Pro Gly Glu Ser Leu Gln Trp Ile Gly
180 185 190
Asn Val Tyr Gly Gly Asn Gly Gly Thr Ser Tyr Asn Gln Lys Phe Gln
195 200 205
Gly Lys Ala Thr Leu Thr Val Asp Lys Ile Ser Ser Thr Ala Tyr Met
210 215 220
Glu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys Ala
225 230 235 240
Arg Arg Pro Val Ala Thr Gly His Ala Met Asp Tyr Trp Gly Gln Gly
245 250 255
Ile Gln Val Thr Val Ser Ser Asp
260

<210> 401
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 401
gttgttgatc agccagttcc ctcaactcca cctacc

36

<210> 402
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 402
gttgttttcg aaggatccgc gtccacctcc gccatgacaa caga

44

<210> 403
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

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<223> oligonucleotide primer

<400> 403
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<210> 404
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 404
gttgtagat ctggagccca aatcttgta caaactcac acatg 45

<210> 405
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide primer

<400> 405
gttggtgatc cttcgaacc gttcctggtg ctgctgcact cgggtgctg 48

<210> 406
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 406
gttggtatcg atctcgagtt atcaggacgc ttcggaggta gatgcgtc 48

<210> 407
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 407
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agcgagctga ccgagctcaa gttcctatgc ctcgggcgcg tgggcaagcg caagctggag 120
cgctgtcaga gcggcctaga cctcttctcc atgctgctgg agcagaacga cctggagccc 180
gggcacaccg agctcctgcg cgagctgctc gcctccctgc ggcgccacga cctgctgcgg 240
cgctgcgacg acttcgaggc gggggcgggc gccggggccg cgcctgggga agaagacctg 300
tgtgcagcat ttaacgtcat atgtgataat gtggggaaag attggagaag gctggctcgt 360
cagctcaaag tctcagacac caagatcgac agcatcgagg acagataccc ccgcaacctg 420
acagagcggtg tgcgggagtc actgagaatc tggaagaaca cagagaagga gaacgcaaca 480
gtggcccacc tgggtggggc tctcagggtc tgccagatga acctggtggc tgacctggta 540
caagagggtc agcaggcccg tgacctccag aacaggagtg gggccatgtc cccgatgtca 600
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<210> 408

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<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> fusion polypeptide

<400> 408

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Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly
20      25      30
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
35      40      45
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
50      55      60
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
65      70      75      80
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly
85      90      95
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly
100     105     110
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys
115     120     125
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val
130     135     140
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr
145     150     155     160
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val
165     170     175
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
180     185     190
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser
195     200     205
Glu Ala Ser
210

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<210> 409

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 409

gttggtgatc ctcccttttg ggtgctggtg gtggttggtg tcctggcttg ctatagcttg 60

<210> 410

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 410

gttggttcga acccagaaaa taataaaggc cactgttact agcaagctat agcaagccag 60

<210> 411

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

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<211> 33
<212> DNA
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<220>
<223> oligonucleotide

<400> 412
gttggttcga acccagaaaa taataaaggc cac 33
<210> 413
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 413
gttggtggatc ctctgctcc catcctgg 28
<210> 414
<211> 32
<212> DNA
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<220>
<223> oligonucleotide

<400> 414
gttggttcga acggcaaagc agtaggtcag gc 32
<210> 415
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 415
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<210> 416
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 416
gttggttatcg atctcgagtc agggtgtttc tgaggaagac ac 42
<210> 417
<211> 645
<212> DNA
<213> Artificial Sequence

<220>
<223> fusion polynucleotide

<400> 417

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ctggagcgcg tgcagagtgg cctggacctg ttcacgggtg tgctggagca gaacgacctg 180
gagcgcgggc acaccgggct gctgcgcgag ttgtgacctg cgctgcgccg acacgatcta 240
ctgcagcgcc tggacgactt cgaggcgggg acggcgaccg ctgcgcccc gggggaggca 300
gatctgcagg tggcatttga cattgtgtgt gacaatgtgg ggagagactg gaaaagactg 360
gcccgcgagc tgaaggtgtc tgaggccaag atggatggga ttgaggagaa gtacccccga 420
agtctgagtg agcgggtaag ggagagtctg aaagtctgga agaattgctga gaagaagaac 480
gcctcgggtg ccggactggt caaggcgctg cggacctgca ggctgaatct ggtggctgac 540
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gattcaactg tgtcttcctc agaaacaccc tgactcgaga tcgat 645

<210> 418
<211> 210
<212> PRT
<213> Artificial Sequence

<220>
<223> fusion polypeptide

<400> 418
Val Asp Pro Ser Asn Met Asp Pro Phe Leu Val Leu Leu His Ser Leu
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20 25 30
Arg Glu Arg Val Ser Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu
35 40 45
Asp Leu Phe Thr Val Leu Leu Glu Gln Asn Asp Leu Glu Arg Gly His
50 55 60
Thr Gly Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu
65 70 75 80
Leu Gln Arg Leu Asp Asp Phe Glu Ala Gly Thr Ala Thr Ala Ala Pro
85 90 95
Pro Gly Glu Ala Asp Leu Gln Val Ala Phe Asp Ile Val Cys Asp Asn
100 105 110
Val Gly Arg Asp Trp Lys Arg Leu Ala Arg Glu Leu Lys Val Ser Glu
115 120 125
Ala Lys Met Asp Gly Ile Glu Lys Tyr Pro Arg Ser Leu Ser Glu
130 135 140
Arg Val Arg Glu Ser Leu Lys Val Trp Lys Asn Ala Glu Lys Lys Asn
145 150 155 160
Ala Ser Val Ala Gly Leu Val Lys Ala Leu Arg Thr Cys Arg Leu Asn
165 170 175
Leu Val Ala Asp Leu Val Glu Glu Ala Gln Glu Ser Val Ser Lys Ser
180 185 190
Glu Asn Met Ser Pro Val Leu Arg Asp Ser Thr Val Ser Ser Glu
195 200 205
Thr Pro
210

<210> 419
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide

<400> 419
gttgtggatc cttcgaacat ggagaacaac aaaacctcag tggattca

48

<210> 420
<211> 44
<212> DNA
<213> Artificial Sequence

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<220>

<223> oligonucleotide

<400> 420

gttgttatcg atctcgagct agtgataaaa gtacagttct ttcg

44

<210> 421

<211> 46

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 421

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46

<210> 422

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 422

gttgttatcg atctcgagtc attagggagg gaagaagagc ttcttccg

48

<210> 423

<211> 45

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 423

gttggtgatc cttcgaacat ggagaacact gaaaactcag tggat

45

<210> 424

<211> 48

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 424

gttgttatcg atctcgagtt agtgataaaa atagagttct tttgtgag

48

<210> 425

<211> 45

<212> DNA

<213> Artificial sequence

<220>

<223> oligonucleotide

<400> 425

gttggtgatc cttcgaacat ggacttcagc agaaatcttt atgat

45

<210> 426

<211> 48

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49076.000004pct2 10.207.655 Seq List Text 07.24.03.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<400> 426

gttggtatcg atgcatgctc aatcagaagg gaagacaagt ttttttct

48

18

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